

JOHN J. WIENS (Editor). 2000. **Phylogenetic Analysis of Morphological Data**. (ISBN 1-56098-841-X, hbk.; 1-56098-816-9, pbk.). Smithsonian Institution Press, PO Box 960, Herndon, VA 20172-0960 U.S.A. (Orders: MLitts@siipress.si.edu, 1-800-782-4612; 202-287-3738 x343). \$49.95 hbk., 26.95, pbk., 220 pp., tables and numerous figures, 6" × 9".

What ever happened to morphology-based systematics? A perusal of titles of such traditional journals as *Systematic Botany* reveals that studies employing morphological data have been replaced largely by those focusing on molecular. If that has you feeling depressed, a quick read-through of this book will have you pumped up about the future of morphological studies.

A symposium, "Morphological Data in Phylogenetic Analysis: Recent Progress and Unresolved Problems," at the 1996 annual meeting of the Society of Systematic Biologists gave birth to this collection of papers. The symposium's title clearly reflects the theme of the book—no hand wringing over the demise of morphology as a science. Instead, the controversy is mentioned in the first contribution (**Chapter 1**, "Molecules Versus Morphology in Systematics") as a means of placing morphological analyses in the perspective of the current state of systematics and providing a context for the rest of the papers. The senior author, David M. Hillis (with John Wiens as junior author), is a prominent advocate of using both morphological and molecular data in systematics. Hence, a reasoned argument is made that the best studies take advantage of the strengths and avoid the weaknesses of both morphological and molecular data. Moreover, graduate training in systematics should generate researchers who have a command of both methods.

In **Chapter 2**, "Character Selection and the Methodology of Morphological Phylogenetics," Steven Poe and John Wiens begin the study of morphological data sets in earnest. In trying to answer the question of how systematists decide on the set of characters they actually include in cladistic studies, the authors surveyed 23 journals between 1987 and 1997 for research papers that explicitly state criteria for character inclusion. Only about 20 percent of the papers gave any criteria, which can be categorized as: 1) excessive variation in terminal taxa, 2) variation continuous and/or character quantitative, 3) missing data, 4) too much homoplasy in character, and 5) polarity unknown. They point out that rejection of characters generally was based on assumptions rather than on empirical evidence. After analyzing each of the criteria, they recommend excluding characters only after one has objective evidence to support rejection.

Chapter 5 ("Coding Morphological Variation within Species and Higher Taxa for Phylogenetic Analysis") actually follows in logical sequence after Chapter 2. However, because its sole author is John Wiens, its placement probably reflects modesty. The first part of the paper focuses on variation within species. Using simulations of an artificial (i.e., "known") phylogeny and congruence analyses of a real data set, he compared the effect of eight different coding methods under parsimony algorithms to that of continuous data under maximum likelihood, as well as under all combinations of three different clustering methods (UPGMA, neighbor-joining, Fitch-Margoliash) with two distance measures (Nei's, Cavalli-Sforza & Edwards's). The results were surprising. The most highly resolved, and potentially most accurate, cladograms resulted from parsimony of continuous characters coded as frequencies and from the non-parsimony methods. Lowest resolution came from excluding all polymorphic characters (i.e., the standard practice of phylogenetics) and from coding the character as missing or equivocal for two or more states. Various coding methods to include data from polymorphic characters (whole species scored apomorphic for any occurrence in the species; species scored according to modal condition; polymorphic condition scored as a state intermediate or alternative to fixed apomorphy) performed at intermediate levels. Wiens therefore concludes that analytical information is lost when polymorphic characters are excluded or not allowed to contribute to tree construction. Wiens also examined the various methods of coding character states in higher taxa

with variation among species. In those cases, he recommends using species as terminals in the analyses rather than coding higher taxa or excluding characters.

The remaining five chapters examine different areas of morphological research in which advances are occurring—morphometrics, ontogeny, hybridization, stratigraphy of fossils, and adaptation.

I find the study of morphometrics (both intraspecific and interspecific variation) to be fascinating and was pleased by Zelditch, Swiderski, and Fink's article (**Chapter 3**, "Discovering Phylogenetic Characters in Morphometric Data). They do a superb job of explaining the field and summarizing its state as practiced today. If one is not familiar with morphometrics, this article would make a good introduction for entering the literature.

Paula Mabee (**Chapter 4**, "The Usefulness of Ontogeny in Interpreting Morphological Characters) summarizes the state of affairs with ontogenetic characters in phylogenetic reconstruction. She reviews the recent history of the role of ontogeny in cladistics, criticizing unjustified uses (especially in pattern cladistics) with recent empirical studies. She also recommends ways of coding ontogeny as characters. However, ontogeny has not proved useful for polarizing or ordering characters or establishing homology. There must first be a better understanding of morphogenesis.

In **Chapter 6** (Hybridization and Phylogenetics: Special Insights from Morphology), Lucinda McDade reviews the state of dealing with hybrids in this context. In particular she discusses the meaning of hybrid intermediacy, how it can be recognized, and the expected placement of hybrids in cladistic analyses. She makes a very good case that new computer algorithms are needed to perform hybrid reticulations in addition to species' cladogenesis.

John Huelsenbeck and Bruce Rannala's treatment of fossil evidence (**Chapter 7**, "Using Stratigraphic Information in Phylogenetics") is enlightening but rather tedious, except for someone interested in maximum-likelihood mathematics. They provide the historical setting for the new interest (since about 1985) of using fossil data for phylogenetics. Rather than focusing on using morphological characters of fossils, they are concerned most with using the stratigraphic occurrences to evaluate or choose among alternative cladograms. Apparently, maximum likelihood statistics have become an important factor in such studies, and they devote a major portion of their article to the topic.

In **Chapter 8** (Logical Problems Associated with Including and Excluding Characters During Tree Reconstruction and Their Implications for the Study of Morphological Character Evolution), Kevin de Queiroz is concerned about circular reasoning. That is, can interpretations about adaptations be related to characters that were included in the tree-building analysis? Despite the importance of avoiding circular reasoning, I found de Queiroz's treatment rather tedious. He spends considerable time building a philosophical basis for evaluating circularity, and more time on the potential circularity of including the data versus excluding the data. He seems to build a straw man of the practice of excluding data to replace it with the superior method of including data. In frustration before reaching his conclusion, I thought to myself, "Why not just do both and compare the effects on the tree?"—to later discover de Queiroz arriving at that same conclusion. Was he actually leading me down that path or did he get there himself by accident?

All in all, the papers are consistently well written and edited. This appears to be an important contribution to the systematic literature and concisely summarizes the advances of and challenges for morphological systematics. I recommend it to anyone wanting to catch up on the cutting edge of morphology or needing encouragement to continue using "out-dated" characters. Perhaps it should be required reading of molecular phylogenetics who have not been trained to recognize the apex of a leaf or the skull of a mammal.—Roger W. Sanders, Associate Collections Manager, Botanical Research Institute of Texas, 509 Pecan Street, Fort Worth, TX 76102-4060, U.S.A., rsanders@brit.org.